

Figure 1. *Arabidopsis thaliana* FAEl promoter:  
(Length: 934 bp)

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-950   ACTCA TAAAACTAG TAGATTGGTT GGTGGGTTTC CATGTACCAG
                                     AtproFW →
-900   AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTTCOC TACTCAATTC
-850   CTAGTTGTGT AAATGATGTG ATATGTAATG CGTATAAAAC GTAGTACTTA
-800   AATGACTAGG AGTGGTTCTT GAGACCGATG AGAGATGGCA GCAGAACTAA
-750   AGATGATGAC ATAATTAAGA ACCAATTTGA AAGGCTCTTA GGTTCGAATC
-700   CTATTCGAGA ATGTTTTTGT CAAAGATAGT GCGGATTTTG AACCAAGAA
-650   AACATTTAAA AAATCAGTAT CCGGTTACGT TCATGCAAAAT AGAAAGTGGT
-600   CTAGGATCTG ATTGTAATTT TAGACTTAAA GAGTCTCTTA AGATTCAATC
-550   CTGGCTGTGT ACAAAACTAC AAATAATATA TTTTAGACTA TTTGGCCTTA
-500   ACTAACTTC CACTCATTAT TTACTGAGGT TAGAGAATAG ACTTGCGAAT
-450   AAACACATTC CCGAGAAATA CTCATGATCC CATAATTAGT CAGAGGGTAT
-400   GCCAATCAGA TCTAAGAACA CACATTCCTT CAAATTTTAA TGCACATGTA
-350   ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT
-300   TGTAGACTTT TTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT
-250   TATTTTAAGT CGAAAACCGA AATTTTCCAT CGAAATATAT GAATTTAGTA
-200   TATATAATTC TCGAATGTAC TATTTTGCTA TTTTGGCAAC TTTGAGTGA
-150   CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT
-100   GTCTAAATGC ATGCTTTTGA AAACGTAACG GACCACAAA GAGGATCCAT
-50   GCAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AACAGAGCA
                                     ← AtproRV
  ATGACGTCCG TTAACGTTAA GTCCTT

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Figure 2. *Brassica napus* FAE1 promoter:  
(Length: 1588 bp)

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-1600 GGTGGGGCAA ATCTGACTTC ACCAAAGAAA CAACTCGAGT CGTTATCCAT
                                     BnproFW →
-1550 CTCCTCATAA GCATCGCTCC ACTCTTTGCC TTCACCGTTT TCGGTTCGGT
-1500 TCTCTACATC GCAACCCGGC CCAAACCGGT TTACCTCGTT GAGTACTCAT
-1450 GCTACCTTCC ACCAACGCAT TGTAGATCAA STATCTCCAA GGTGATGGAT
-1400 ATCTTTTATC AASTAAGAAA AGCTGATCCT TCTCGAAGC GCACGTGCGA
-1350 TGACTCGTCC TGGCTTGACT TCTTGAGGAA GATTCAAGAA CGTTCAGGTC
-1300 TAGGCGATGA AACTCACGGG CCGGAGGGGC TGCTTCAGGT CCTCCCCGG
-1250 AAGACTTTTG CGGCGGCGCG TGAAGAGACG GAGCAAGTTA TCATTGGTGC
-1200 GCTAGAAAAT CTATTCAAGA ACACCAACGT TAACCCTAAA GATATAGGTA
-1150 TACTTGTGGT GAACTCAAGC ATGTTTAATC CAACTCCATC GCTCTCCGG
-1100 ATGGTCGTTA ACACTTTCAA GCTCCGAAGC AAGTAAGAA GCTTTAACCT
-1050 TGGTGGCATG GGTGTAGTG CCGCGGTTAT AGCCATTGAT CTAGCAAAGG
-1000 ACTTGTGCA TGTCCATAAA AATACGTATG CTCTTGTGGT GAGCACAGAG
-950 AACATCACTT ATAACATTTA CGCTGGTGAT AATAGGTCCA TGATGGTTTC
-900 AAATTGCTTG TTCCGTGTTG GTGGGGCCGC TATTTTGCTC TCCAACAAGC
-850 CTGGAGATCG TAGACGGTCC AAGTACGAGC TAGTTCCACG CGTTCCAGCG
-800 CATACCGGAG CTGACGACAA GTCTTTTCTT TCGGTGCAAC AAGGAGACGA
-750 TGAGAACGGC AAAATCGGAG TGAGTTTGTC CAAGGACATA ACCGATGTTG
-700 CTGGTCAAC CGTTAAGAAA AACATAGCAA CGTTGGGTCC GTTGATTCTT
-650 CGTTAAGCG AGAAACTTCT TTTTTCGTT ACCTTCATGG GCAAGAACT
-600 TTTCGAAGAT AAAATCAAC ATTACTAGCT CCGGACTTC AACTTGCTA
-550 TTGACCATTT TTGTATGAT GCGGAGGCA GAGCGTGAT TGATGTGCTA
-500 GAGAAGAACC TAGCCCTAGC ACCGATCGAT CTAGAGGCAT CAAGATCAAC

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Figure 2 Continued *Brassica napus* FAE1 promoter:

Figure 3. *Lunaria annua* *FAE1* promoter:  
(Length: 1069 bp)

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-1100          CG CCGGGGAGTT TCAGCTTAAC CCGTAAAATT
                                     LaproFW →
-1050 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
-1000 TGTTACTCAA TTGGGCTAAG TGTATTATTA TATGTGTTGT ATATAATAAA
-950  GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
-900  TGGCCTCTTA GCTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
-850  GCAAAAATAG AATCAATTT ATAAGTGTTC AACAAATCG ATGGTATAAC
-800  TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG
-750  AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
-700  AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
-650  ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
-600  TTTTATTTGG CACAAACTTG TTTTACTTTT CTACCTTATA AITTGGGAAC
-550  TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG
-500  AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT
-450  CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
-400  TCGGATCAGT ATTCTTAAAT AGAATATAA AACTAATTCA ATAGTTACAG
-350  ATAAAAACTT ATATAGACTT TTTTATTTGG AATATAAAAG TATCAATATA
-300  TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTATATA
-250  TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAATG AATTTTAGTA
-200  TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTT TGGCACCTTT
-150  CATCTGACTA CTAATTTACT TCAATGTGTA TGCATGCATG AGCATCAGTA

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-100 ATACACATGT CTATATAAAT GCATGTAAAA CGTAACGGAC CACAAAAGTG
-50 GATCCATACA AATACATCTC ATCGCACCGT CTCCGACACA AAAGTGAACA
      ← LaproRV
 1 ATGACGTCTG TGAACGTAAG ACTCGTTTAC GATTACGTCA TATCCAACTT
51 TTTCAACCTG TTTTCTTCC CAATGACGGG GATCGTCGCC GGAAAAGGCT
      ← Lawalk2
101 CTCGTCTTAC CACAAACGAT CTCCACCA
      ← Lawalk1

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Page 1 \*\*\*\*\*SECRET\*\*\*\*\*

[illegible]

CE3

A. c. CATAATTAGTCAGAGGGTATG-----CCCAATCAGATCTAAGAACACACATTCCCTG  
L. a. CATAATTAGTCAGAGGCTAGGGAGATTCCAGCCAATCAATGCTAACAAACAAA-ATTCTCTT  
B. n. CCGATCGATGTAGAGGC-----ATCAAGATCAAGCTTAGCATAGATTTGG  
\* \* \* \* \*  
Con. 4 CMKAWYKAKKYAGAGGSSNNNNNNNNNNNNNNNNNNATCARDDYYAASRWYAMANAkWYYYKB

A. c. AA--ATTTTA--ATGCAC-ATGTAATCAT-----AGTTT-----AGCACAAATTCAAAA  
L. a. AATGATCTAACGATGCT--ATTTAATATTCCGATCAGTATTCTTAAATAAGAATATAAAA  
B. n. AAACACTTCATCTAGCTCAATATGGTATG-----AGTTGGCATACAT-AGAAG-CAAAA  
\* \* \* \* \*  
Con. 4 AANNAYYTHANNWGWGWNNAATDTRRTMWKNNNNNNNAGTWKNNNNNNNAKNASAAKNYAAAA

A. c. ATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT----TTGGCST-TAAAGG  
L. a. CTAATTCGAATAGTTACAGATAAAAACTTATATAGACTTTTTTAT--TTGGAATATAAAAG  
B. n. GGAAGGATGAA-GAAAGGTAATAAAGTTTGGCAGATTGCTTTAGGGTCAGGCTTTAAGTG  
\* \* \* \* \*  
Con. 4 VKAAKKHWRWANKWAMRGWHADAAAABTTDKRNNGAYTKYTTTNNNNNTYRGVVTNTAARDG

A. c. AA-----GACTAAGTTTATA-CGT-----ACATTT-TATTTTAAAGT  
L. a. TATCAATATATTATA-GACAATATTTATAACGTTAAAAATACATATTTTATATTTTTTAT  
B. n. TAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTCGACAAATAGTCCTTGGGA  
\* \* \* \* \*  
Con. 4 WANNNNNNNNNNNNNNNGWSDMWVTWWAYANYGTNNNNNNNNNNNAYAWWTNKWYTTDDRW

CE1

A. c. GGA-----AAACCGAAATT--TTCCATCGAAATATATGA--ATTT-AGTATAT----  
L. a. ATATTTATTTCAAATTGAAAAGCATTACTTCTATCGAAATGA--ATTTTAGTATATTTAT  
B. n. ACACT-----GCATCGACAGATACCCGGTCAAAATTGATTCTGATTGAGSTAAGTCAGA  
\* \* \* \* \*  
Con. 4 RBAYTNNNNNNRMAYYGAYADDYAYYMSDTCDAWMKWDA TKMNNATTYNRGTAWRNTNNNN

G-box2

A. c. --ATATTTCTGCAAT-----GTACTATTTTGGTATTTTGGCAA-CTTCAGTGGACTAC  
L. a. TAATATTTTTTTAATC-----GGACTACTTTTCTATTTTGGCAC-CTTCATCTGACTAC  
B. n. GACTCGTGTCCAAAACGCTCGCTCTTAATAAAGCATGTTTGGCTCTTTTCTGTTT--CTTT  
\* \* \* \* \*  
Con. 4 NNM TMKTKYYBHAAWN NNNNNNGKMC TAHTWWVCKATKTTGCGWMNCTTTCRKYKNNCTWY

G-box1

A. c. TACTTTATTACAATGTGT--ATGGATGC-ATGAG--TTTGAGTA-TACACATGTCTAAA  
L. a. TAATTTATTTCAATGTGT--ATGCATGC-ATGAG--CATGAGTAATACACATGTCTATA  
B. n. TTATTTGTTATAATAATTGATGGCTACGATGTTTCTCTTGTGTTTGTATGAATAAAGAA  
\* \* \* \* \*  
Con. 4 TWMTTTRTTWYAATRWKTNNAATGSMTRCNATGWNKNNNYWTGWNTRWTAYRMA TRWMKAWW

A-box 1

A. c. TGCATGCT-TTGCAAAACGTAACGGGACC-ACAAAAGAGGATCCATGGGAAATACATCTCAT  
L. a. TAAATGCA-T-GTAAAACGTAACGGGACC-ACAAAAGTGGATCCATACAAATACATCTCAT  
B. n. GCAATCGTGTCTTATGATTTTGTATGTTTACATCTATGATCTCTT-ATTTCATGAAT  
\* \* \* \* \*  
Con. 4 KVMATGSWNTNSYARWAYKTRAYKSWYNNACAWRWRWGKATCYMTDNAWWTACATSKMAT

A. c. AGC-TTCCTCCATTATTTTCCGACACAAAA-CAGAGCA---  
L. a. CGC-ACCCTC-----TCCGACACAAAACGGAACA---  
B. n. TTTTAAACGCC-----TAAAAAAAACGGAAATCCG  
\* \* \* \* \*

Con. 4 HKYNWVHMCCKNNNNNNNNNTMMRAMAMAAAACDGAARYWNNN

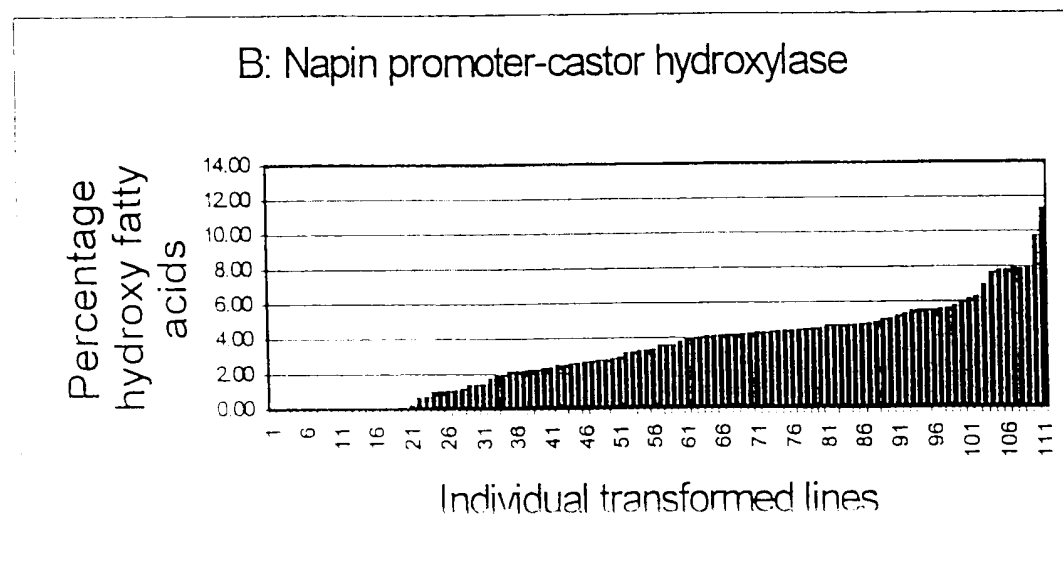
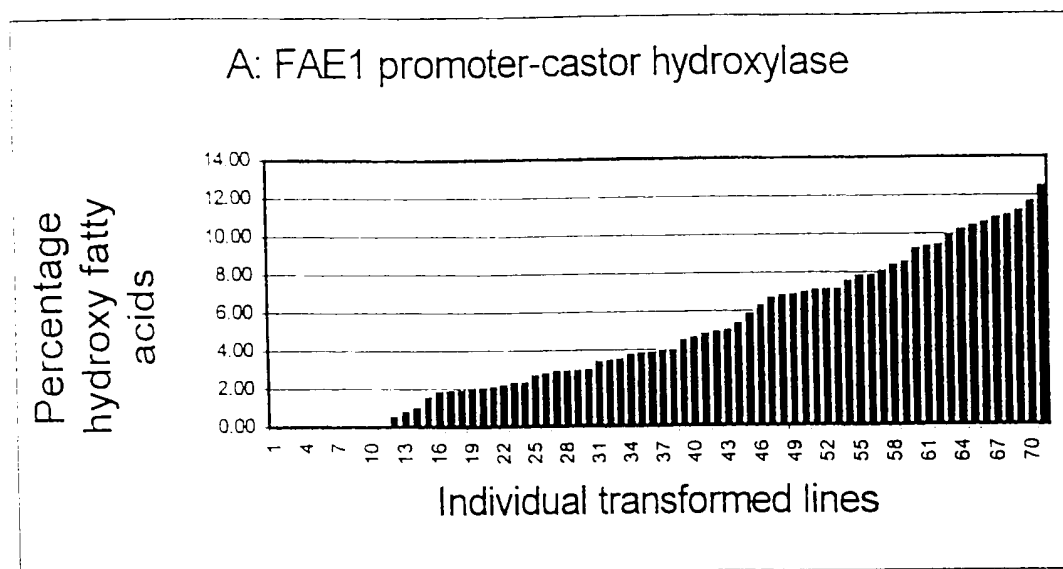




Figure 5 Continued: Alignment of *A.t.* and *L.a.* *FAE1* promoters

<i>A.t.</i>	-381	CACATTCCCTCAA--ATTTTA--ATGCACATGTAATCAT-----AGTTT-----AGCA
<i>L.a.</i>		AA-ATTCTCTTAATGATCTAACGATGCT-ATTTAATATTCGGATCAGTATTCTTAAATAA
<i>Con.5</i>		MANATTCTCTYAANNATYTWANNATGCWNATKTAATMWTNNNNNNAGTWTNNNNNNNAKMA
<i>A.t.</i>	-337	CAATTCAAAAATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT--TTGGCG
<i>L.a.</i>		GAATATAAACTAATTCAATAGTTACAGATAAAAACTTATATAGACTTTTTTATTTGGAA
<i>Con.5</i>		SAATWYAAAAMTAATKYARTANTTAMAGAYAAAAYTTRTANNGACTTTTTTNNNTTGGMR
<i>A.t.</i>	-232	T-TAAAGGAA-----GACTAAGTTTATA-CGT-----ACATTT-TAT
<i>L.a.</i>		TATAAAAGTATCAATATATTATAGACAAATTTTATAACGTTAAAAATACAATATTTATAT
<i>Con.5</i>		TNTAAARGWANNNNNNNNNNNNNGACWAWRTTTATANCGTNNNNNNNNNNAYATTTNTAT
<i>A.t.</i>	-247	TTTAAGTGGA-----AAACCGAAATT--TTCCATCGAAATATATGAATTT-AGTATA
<i>L.a.</i>		TTTTTATATATTTTATTTCAAATTTGAAAAGCATTACTTCTATCGAAATGAATTTTAGTATA
<i>Con.5</i>		TTTWWRTRKANNNNNNNNNAAAYYGAAAWKNNTTMCWTCKAWMKAWATGAATTTNAGTATA
<i>A.t.</i>	-198	T-----ATATTTCTGCAAT-GTACTATTTTGCTATTTTGGCAACTTTTCAGTGGACTACT
<i>L.a.</i>		TTAATTAATATTTTTTTAATCGGACTACTTTTCTATTTTGGCACCTTTTCATCTGACTACT
<i>Con.5</i>		TNNNNNNATATTTYTKYAATNGKACTAYTTTSTCTATTTTGGCAMCTTTCAKYKGACTACT
<i>A.t.</i>	-145	ACTTTATTACAATGTGTATGGATGCATGAGTTTGAGTA-TACACATGTCTAAATGCATGC
<i>L.a.</i>		AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATACACATGTCTATATAAATGC
<i>Con.5</i>		AMTTTATTWCAATGTGTATGSATGCATGAGYWTGAGTANTACACATGTCTAWATRMATGC
<i>A.t.</i>	-86	TTTGCAAAACGTAACGGACCACAAAAGAGGATCCATGCAAATACATCTCATAGCTTCCTC
<i>L.a.</i>		AT-GTAAACGTAACGGACCACAAAAGTGGATCCATACAAATACATCTCATCGCACCTTC
<i>Con.5</i>		WTNGYAAAACGTAACGGACCACAAAAGWGGATCCATPCAAATACATCTCATMGCWYCTTC
<i>A.t.</i>	-26	CATTATTTTCCGACACAAA-CAGAGCA
<i>L.a.</i>		-----TCCGACACAAAACCTGAACA
<i>Con.5</i>		NNNNNNNNNTCCGACACAAAACWGAACA

Figure 6



Accession	Sequence	Position
BnFAE1	GGTTGGGCAATCTGACTTCACCAAGAAGAACTCGAGTGGTTTATGCCATCTCTCATATA	60
LaFAE1	-----	
BnFAE1	GCATCGCTCGACTCTTTTCGCTTCACGTTTTTGGGTGCGTTCTCTACATCGCAACCGCGG	120
LaFAE1	-----	
BnFAE1	CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCACCAACCGCATTTGTAGATCAA	180
LaFAE1	-----CGCGGGGAGT-FTCAGCTTAACCGGTAAAAATGGCGCTGTACATATA	186
BnFAE1	GTATCTCCAAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG	240
LaFAE1	TTTACCACCTGAGT-AAAGACATCAGTTAATGATTT-----GTTGTTACTCAATTGGGCT	249
BnFAE1	GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAAGCTTCAGGTC	300
LaFAE1	AAGTGTATTATTATATGTGTTG-----TATATAATAAAGGT---AGAACGT--AAATT	307
BnFAE1	TAGGCGATGAAACTCACGGGGCCCGAGGGGCTGCTTCAGGTGCGTCCCGGGAAGACTTTTG	360
LaFAE1	TA--CTAAGAAATGTGTTTTCCAAATGTGATTGCTCTTTGGCGCTCTTAGGTTTGAATCCTA	365
BnFAE1	CGGCGCGCGCTGAAGAGACGGAGCAAGTTATCATTGGTGGCTAGAAAATCTATTCAAGA	420
LaFAE1	CT-----CGAGAAGACTAATTTTAAAT-TTACTGGCAAAAATAGAAATCAATTTATAA	426
BnFAE1	ACACCAACGTTTAAACCCTAAAGATATAGGTATACCTTGTTGGTGAAGTCAAGCATGTTTAAATC	480
LaFAE1	GTGTTTAAACAAATC--GATGGTATAACTG-ATTAGTGATCACTCTTAGGTT--TTGATC	486
BnFAE1	CAACTCCATCGGCTCTCGCGATGGTGGTTAACACTTTCAAGCTCGGAAGCAACGTAAGAA	540
LaFAE1	CAACTCGAGTATTG-----AGTATTGAACGCTTT-----TTTTAAATAAAATCTTGA	546
BnFAE1	GCTTTAACCTTGGTGGCATGGGTTGTAGTCCCGCGCTTATAGCCATTGATCTAGCAAAAGG	600
LaFAE1	TTTATAAA-TTGGTTTTTTGAGTAAAAAAGTCTTAATAATTTCTCTT-TGTTTTAATGG	606
BnFAE1	ACTTGTTCATGTCC-ATAAAAATACGTATGCTCTTGTGGTGAAGCAGAGAACATCACT	660
LaFAE1	GTTTGTTTTGCATTTTATAAGCTTAAATTTTCTAAATTAAT-ATTTTATCTATCATCTG	666
BnFAE1	TATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGGTTGTTCCGTTT	720
LaFAE1	CGTAAAGTTT-----TATTTGGCACAAACTTGTTTTA---GTTTTCTACCTTATA	726
BnFAE1	GTGGGGGCTATATTTTCTCTCTCAAGCAAGGCTGAGATCTTAGACGCTCAAGTACGAG	780
LaFAE1	ATTTGGGA-ACTGGTTGAGTCA-----AAGCGTACCGGACAAATATCTTTATATTC	786
BnFAE1	GTAGTTTACACGGTTTCAACGCATACCGGAGCTGAGCAGCAAGTCTTTTGGTTTCGTTGCAA	840
LaFAE1	-TTATTTA-AGAAATTAACACTCATCTCATAATTAGTCAGAGGC-----TAGGGAGATT	846
BnFAE1	CAAGGAGACGATGAGAACCGCAAAATCGGAGTGAGTTTGTCCAAAGGACATAACCGATGTT	900
LaFAE1	CAGCCAATCAATGCTAACAACAAAAATCTCTTAA--TGATCTAACGATGCTATTTAATAT	906

Figure 7 Continued: Alignment of *B.n.* and *La.* *FAE1* promoters

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BnFAE1      GCTGGTCGAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTCGGTTA-AG 958
LaFAE1      TCGGATCAGTATTCTTAAATAAGAATATAAA-----ACTAATTCAATAGTTACAG 732
      * * * * *

BnFAE1      CGAGAAACTTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATAAAATCAA 1018
LaFAE1      ATAAAAACTTATATAGACTTTTTTATTTG-GAATATAAAAGTATCAATATATTATAGACA 791
      * * * * *

BnFAE1      ACATTACTACGTCGCGGATTTCAAACCTTCTATTGACCAATTTTGATACATGCCGGAGG 1078
LaFAE1      ATATTTATA-----ACGTTAAAAATACAAATTTATATTTTATATATTTTTCAAA 845
      * * * * *

BnFAE1      CAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCACCGATCGATGTAGAGGC 1138
LaFAE1      TTGAAAAGCATTACTTCTATCGAAATGAATTTTAGT-----ATATTAATTAATATTTT 901
      * * * * *

BnFAE1      ATCAAGATCAACGTTACATAGATTTGGAACACTTCATCTAGCTCAATATGGTATGAGTT 1198
LaFAE1      AATCGGACTACTTTCTAT----TTTGGCACCTTTCATCTGACT-----ACT 944
      * * * * *

BnFAE1      GGCATACATAGAAGCAAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTT 1258
LaFAE1      AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATA-----CACATGTCTAT 996
      * * * * *

BnFAE1      AGGGTCAGGCTTTAAGTGTAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTC 1318
LaFAE1      ATAAATGCATGTAAAACGTAACGG-ACCACAAAAGTGGATCCATACAAATACATCTCATC 1055
      * * * * *

BnFAE1      GACAAATAGTCCTTGGGAACACTGCATCGACAGATACCGGTCAAAATTGATTCTGATT 1378
LaFAE1      G-CACCCCTCTCCGACACAAAACGTAACA----- 1082
      * * * * *

BnFAE1      AGGTAAGTCAGAGACTCGTGTCCTAAAACGGTCGGTCCTAATAAACGATGTTTGCTCTCT 1438
LaFAE1      -----

BnFAE1      TCGTTTCTTTTATTTGTTATAATAATTTGATGGGTACGATGTTTCTCTTGTGTTATG 1498
LaFAE1      -----

BnFAE1      AATAAAGAAATGCAATGGTGTCTAGTATTTGATGTTTTACATGATGATCTCTTATTT 1558
LaFAE1      -----

BnFAE1      ACATGAAATTTTAAACGGCTAAAAAAGGGAATTCGG 1600
LaFAE1      -----

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Figure 8: Alignment of *B.n.* and *A.t.* *FAEI* promoters

CLUSTAL W (1.81) multiple sequence alignment

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AtFAE1      -----
BnFAE1      GGTGGGCAATCTGACTTCACCAAGAAACAACTCGAGTCGTTATCCATCTCTCATAA 60

AtFAE1      -----
BnFAE1      GCATCGGTCCACTCTTTCCCTTCACCGTTTTGGTTGGTTCTCTACATCGCAACCCCGC 120

AtFAE1      -----
BnFAE1      CCAAACCGGTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180

AtFAE1      -----ACTCATAAA 10
BnFAE1      GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGGTGATCTCTCTCGGAACG 240
              *** **

AtFAE1      ACTAGTAGATTGGTTGGT--TGGTTTCCATGTACCAGAAGGCTT-----ACCTATTAGT 63
BnFAE1      GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAACGTCAGGTC 300
              *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      TGAAAGTTGAAACTT-TGTTCCCTACT--CAATTCCTAGTTGTGTAATGTATGTATATG 120
BnFAE1      TAGGCGATGAAACTCACGGGCCGAGGGGCTCCTTCAGGTCCCTCCCGGAAGACTTTTG 360
              *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

AtFAE1      TAATG-CGTATAAAACGTAGTACTTAAATGACTAGGAGTGGTTCTTGAGACCGATGAGAG 179
BnFAE1      CGGCGGCGCGTGAAGAGACGGAGC-AAGTTATCATTGGTGGCGGTAGAAAATCTATTCAAG 419
              *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      A----TGGGAGCAGAACTAAAGATGATGACATAATTAAGAACGAATTTGAAAGGCTCTTA 235
BnFAE1      AACACCAACGTTAACCCCTAAAGATATAGGTATACTTGTGG-TGAAGTCAAGCATGTTTAA 478
              *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

AtFAE1      GGTITGAATCCTATTGAGAAATGTTTTGTCAAAGATAGTGGCGA-TTTGAACCAAGA 294
BnFAE1      ---TCCAAGTCCATCGCTCTCCCGCATGGTCTTAACACTTTCAGGCTCGAAGCAACGT 535
              *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      AAACATTTAAAAATCAGTATCC--GGTTAC-GTTCATGCAA-ATAGAAAGTGGTCTAGG 350
BnFAE1      AAGAAGCTTTAACCTTGGTGGCATGGGTTGTAGTGGCGCGCTTATAGCCATTGATCTAGC 595
              **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      ATCTGATTGTAATTTTAGACTTAAAGAGTCTCTTAAGATTCAATCCTGGCTGTGTACAAA 410
BnFAE1      AAAGGACTT--GTTGCATGTCCATAAAAAATACGTATGCTCTTGTGGTGAGCACAGAGAAC 553
              *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

AtFAE1      ACTACAAATAATATAT---TTTAGACTATTTGGCTTAACTAACTTCCACTCATTATTT 467
BnFAE1      ATCATTATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTC 713
              *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

AtFAE1      -----
BnFAE1      CGTGTGGTGGGGCGGCTATTTGCTCTCCAACAAG--CGTGGAGATCGTAGACGCTCCA 771
              **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      -----CE3-----
BnFAE1      ATAAATTAGTCAGAGGGGTATG--CCCATCAGATCTAAGAACACACATTCCCTCAATTTTA 584
              AGTACGAGCTAGTTCAACACGGTTGGAACGCATACCGGAGCTGACGACAAGTCTTTTCTT 831
              *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

AtFAE1      ATGCACATGTAATCATAGTTTAGCACAAATCAAAAATAATGTAGTATTAAGACAGAAAT 544
BnFAE1      CGGTGCAACAAGGAGACGATGAGAACGGCAAAATCGAGTGAGTTTGTCCAAGGACATAA 991
              *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

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Figure 8 Continued: Alignment of *B.n.* and *A.L.* *FAE1* promoters

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AtFAE1      TTGTAGACTTTTTTTGGCGTTAAAGGAAGACTAAG-----TTTATACGTACATTTTAT 698
BnFAE1      CCGATGTTGCTGGTGGACCGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTC 951
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      T-TTAAGTGGAACCCGAAATTTTCCAT-----CGAAATATATGAATTTAGTATATATA 751
BnFAE1      CGTTAAGCGAGAACTTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATA 1011
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

                                     G box 2
AtFAE1      TTTCTGCAATGTACTATTTTGCTATTTTGGCAACTTTCAGTGGACTACTCTTAT-TAC 810
BnFAE1      AAATCAAACATTACTACGTCCCGGATTTCG-AACTTGCTATTGACCATTTTGTATACAT 1070
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

                                     G-box 1
AtFAE1      AATGTGTATGGATGCATGAGTT-TGAGTATACACATGTCTAAATGCATGCTTTGCAAAAC 869
BnFAE1      GCCGGAGGCAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCAGCGATCGAT 1130
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      GTAACGG-ACCACAAAAGAGGATCCAT-----GCAAATACATCTCATAGCTTCCTCCAT 922
BnFAE1      GTAGAGGCATCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGG 1190
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      TATTTTCCGACACAAACAGA-GCA----- 945
BnFAE1      TATGAGTTGGCATACATAGAAGCAAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAG 1250
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1      -----
BnFAE1      ATTGCTTTAGGGTCAGGCTTTAAGTGTAAAGTGCAGTTTGGGTGGCTCTAAACAATGTC 1310

AtFAE1      -----
BnFAE1      AAAGCTTCGACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAAATTGAT 1370

AtFAE1      -----
BnFAE1      TCTGATTGAGGTAAAGTCAGAGACTCGTGTCAAAACGGTCGGTCTAATAAACGATGTTT 1430

AtFAE1      -----
BnFAE1      GCTCTCTTCTGTTTCTTTTATTGTTATAATAATTGATGGCTACGATGTTTCTCTTGT 1490

AtFAE1      -----
BnFAE1      TTGTTATGAATAAAGAAATGCAATGGTGTCTAGTATTGATTGTTTACATGTATGTATC 1550

AtFAE1      -----
BnFAE1      TCTTATTTACATGAAATTTTAAACGGCTAAAAAAGGAAATTCGG 1600

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